

SUBSTITUTE SHEET (RULE 26)

### <u>2/24</u>

		10	20	30	40	50	
MOUSE-X1.DNA	1	ATGAGGCTTC	CTGGTTGGTT	GTGGCTGAGT	TCTGCCGTCC	TCGCTGCCTG	50
HUMAN-X1.DNA	1	ATGAAGCTGG	CTAACTGGTA	CTGGCTGAGC	TCAGCTGTTC	TTGCCACTTA	50
		60	70	80	90	100	
MOUSE-X1.DNA	51	CCGAGCG	GTGGAGGAGC	ACAACCTGAC	TGAGGGGCTG	GAGGATGCCA	100
HUMAN-X1.DNA	51	CGGTTTTTTG	GTTGTGGCAA	ACAATGAAAC	AGAGGAAATT	AAAGATGAAA	100
		110	120	130	140	150	
MOUSE-X1.DNA	101	GCGCCCAGGC	TGCCTGCCCC	GCGAGGCTGG	AGGGCAGCGG	GAGGTGCGAG	150
HUMAN-X1.DNA	101	GAGCAAAGGA	TGTCTGCCCA	GTGAGACTAG	AAAGCAGAGG	GAAATGCGAA	150
		160	170	180	190	200	
MOUSE-X1.DNA	151	GGGAGCC	AGTGCCCCTT	CCAGCTCACC	CTGCCCACGC	TGACCATCCA	200
HUMAN-X1.DNA	151	GAGGCAGGGG	AGTGCCCCTA	CCAGGTAAGC	CTGCCCCCCT	TGACTATTCA	200
		210	220	230	240	250	
MOUSE-X1.DNA	201	GCTCCCGCGG	CAGCTTGGCA	GCATGGAGGA	GGTGCTCAAA	GAAGTGCGGA	250
HUMAN-X1.DNA	201	GCTCCCGAAG	CAATTCAGCA	GGATCGAGGA	GGTGTTCAAA	GAAGTCCAAA	250
		260	270	280	290	300	
MOUSE-X1.DNA	251	CCCTCAAGGA	AGCAGTGGAC	AGTCTGAAGA	AATCCTGCCA	GGACTGTAAG	300
HUMAN-X1.DNA	251	ACCTCAAGGA	AATCGTAAAT	AGTCTAAAGA	AATCTTGCCA	AGACTGCAAG	300
		310	320	330	340	350	
MOUSE-X1.DNA	301	TTGCAGGCTG	ACGACCATCG	AGATCCCGGC	GGGAATGGAG	GG	350
HUMAN-X1.DNA	301	CTGCAGGCTG	ATGACAACGG	AGACCCAGGC	AGAAACGGAC	TGTTGTTACC	350
		360	370	380	390	400	
MOUSE-X1.DNA	351	-AATGGA	GCAGAGA	CAGCCGAGGA	CAGTAGAGTC	CAGGAACTGG	400
HUMAN-X1.DNA	351	CAGTACAGGA	GCCCCGGGAG	AGGTTGGTGA	TAACAGAGTT	AGAGAATTAG	400
		410	420	430	440	450	
MOUSE-X1.DNA	401	AGAGTCAGGT	GAACAAGCTG	TCCTCAGAGC	TGAAGAATGC	AAAGGACCAG	450
HUMAN-X1.DNA	401	AGAGTGAGGT	TAACAAGCTG	TCCTCTGAGC	TAAAGAATGC	CAAAGAGGAG	450
		460	470	480	490	500	
MOUSE-X1.DNA				CCTGGAGACG			500
HUMAN-X1.DNA	451			CCTGGAGAAG			500
		510	520	530	540	550	
MOUSE-X1.DNA				ACAACAAAGT			550
HUMAN-X1.DNA	501			ACAGCAAAGT			550
		560	570	580	590	600	
MOUSE-X1.DNA				TGTTCCAAGT	=		600
HUMAN-X1.DNA	551			TGTTCAAAGT			600
		610	620	630	640	650	
MOUSE-X1.DNA		CAGTCACAGC		• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • •	• • • • • • • • • •	650
HUMAN-X1.DNA	601	CAGTCACGTC	CAG				650

				20	40	50	
		10	20	30		• •	50
MOUSE-X2.DNA	1	TTCAACATCT	AATATACAAA	GATTGTTCCG	ACCACIACGI	AATACCCAAA	50
HUMAN-X2.DNA	1	TTCAACATCT		SATTGCTCTG 80	90	100	50
		60	70		• •		100
MOUSE-X2.DNA	51	AGAAGCAGTG	GGGCCTACAG	AGTTACCCCT	CATCACAGAA	ACAGCAGCII	100
HUMAN-X2.DNA	51	AGAAGCAGTG			140	150	100
		110	120	130			150
MOUSE-X2.DNA	101	TGAGGTCTAC	TGTGACATGG	AGACCATGGG	TGGAGGCTGG	ACGGIGCIGC	150
HUMAN-X2.DNA	101	TGAAGTTTAC			190	200	130
		160	170	190			200
MOUSE-X2.DNA	151	AGGCTCGCCT	TGATGGCAGC	ACCAACTTCA	CCAGAGAGIG	GARAGACIAC	200
HUMAN-X2.DNA	151	AGGCACGTCT			240	250	200
		210	220	230			250
MOUSE-X2.DNA	201	AAAGCCGGCT	TTGGAAACCT	TGAACGAGAA	TTTTGGTTGG	GCAACGATAA	
HUMAN-X2.DNA	201	AAAGCAGGCT					250
		260	270	280	290	300	200
MOUSE-X2.DNA	251	AATTCATCTT	CTGACCAAGA	GTAAGGAAAT	GATTTTGAGA	ATAGATCTTG	300
HUMAN-X2.DNA	251	AATTCATCTT				ATAGATOTIG 350	300
		310	320	330	340	•••	350
MOUSE-X2.DNA	301	AAGACTTTAA	TGGTCTCACA	CTTTATGCCT	TGTATGATCA	GTTTTATGTG	350
HUMAN-X2.DNA	301	AAGACTTTAA				GTTTTATGTG	350
		360	370	380	390	400	400
MOUSE-X2.DNA	351	GCTAATGAAT	TTCTCAAATA	CCGATTACAC	ATCGGTAACT	ACAATGGCAC	400
HUMAN-X2.DNA	351	GCTAATGAGT			GTTGGTAACT	ATAATGGCAC	400
		410	420	430	440	450	450
MOUSE-X2.DNA	401	GGCAGGGGAT	GCCTTGCGTT	TCAGTCGACA	CTACAACCAT	GACCTGAGGT	450
HUMAN-X2.DNA	401	AGCTGGAGAT				500	450
		460	470		490		500
MOUSE-X2.DNA	451	TTTTCACAAC	CCCAGACAGA	GACAACGATC	GGTACCUCTC	TGGGAACTGI	500
HUMAN-X2.DNA	45	TTTTCACCAC			GATATCCTTC	TGGGAACTGT 550	300
		510			540		550
MOUSE-X2.DNA	50:	GGGCTCTAT	: ACAGCTCAGG	CTGGTGGTTT	GATTCATGTC	TCTCTGCCAA	550
HUMAN-X2.DNA	50	L GGGCTGTACT				600	330
		560			• • • •		600
MOUSE-X2.DNA	55	1 CTTAAATGG	AAATATTACO	ACCAGAAATA	CAAAGGTGTC	CGTAATGGGA	600
HUMAN-X2.DNA	55	1 CTTAAATGG				650	600
		611					650
MOUSE-X2.DNA	60	1 TTTTCTGGG	G CACCTGGCC	r GGTATAAACC	AGGCACAGCC	AGGTGGCTAC	650
HUMAN-X2.DNA	60	1 TTTTCTGGG				TGGTGGCTAC 700	050
		66	0 676				700
MOUSE-X2.DNA	65	1 AAGTCCTCC	T TCAAACAGG	CAAGATGATG	ATTAGGCCCA	AGAATTTCAA	700
HUMAN-X2.DNA	65	1 AAGTCCTCC				AGCACTTIAA 750	.00
		71	-	0 730	/40	, , , , , ,	750
MOUSE-X2.DNA	70	1 GCCATAA					750
HUMAN-X2.DNA	70	1 GCCATAA					150

10	20	30	40	50	60
		AGGTATTCGT	TATCTAATAG	GGCAATTAAT	TCCTTCAGCA
70	80	90	100	110	120
• -		CATATTTTTC	ATAGCTAAAA	AATGCCTTGT	TTCATATTTT
130	140	150	160	170	180
TCATAGCTAA	AAAATGATGT	CTGACGGCTA	GGTTCTTATG	CTACACAGCA	TTTGAAATAA
190	200	210	220	230	240
AGCTGAAAAA	CARTGCATTT	TAAAGGAGTC	CTTTGTTGTT	ATGCTGTTAT	CCAATGAACA
250	260	270	280	290	300
CTTGCAAGCA	ATTAGCAATA	TTGAGAATTA	TACATTAGAT	TTACAATTCT	TTTAATTTCT
310	320	330	340	350	360
ATTGAAACTT	TTTCTATTGC	TTGTATTACT	TGCTGTATTT	TAARAAAAA	TGTTGGCTGG
370	380	390	400	410	420
GTGTGGTAGC	TCACGCCTGT	AATNCCAGCA	CTTTGGAATG	TCAAGGCAGG	CAGATCACTT
430	440	450	460	470	480
GAGGTCAGGA	GTTTGAGACC	AGCCTGGCCA	AACATGTGAA	ACGCTGTNTN	TATTAAAAAT
490	500	510	520	530	540
ACAAAAATTA	GCCGGGCATG	GTGGNACATG	CCTGTAATCC	TAGNTACTTG	
550	560	570	580	590	600
GCAGGAGAAT	CGCTTGAACC	TGAGAGGAAG	AGGTTGCAGT	GAGCCAAGAA	
610	620	630	640	650	660
CACTCCAGCA	TGGGTGACAG	AGAAAACTCT		AAAAAATAAT	
670	680	690	700	710	720
CAGTAGGNTG	GATTCTACAC	AAAGTAATCT			GCACATCTGA
730	740	750	760	770	780
AGGTATATCA		GCTATAATTA			
790		- <del>-</del> -		830	840
AATCTATATC	_		ACCCTACAGO		
850					900
GGAACTAATA					
910					
		ATGTGGTAGO			
970			_		
CAATGTAACI	·	GGGTTTAAAG			
1030					1000
ATGTTTGAT	TTGAAAACT	3 CTTTAACAT	* AA	• • • • • • • • •	• • • • • • • • •

3'UTR of hfgl2. The A at position 1 corresponds to position 1354 on the cDNA.

### <u>5/24</u>

		10	20	30	40	50	
MOUSEPRO.AMI	1	REPGALALS	SAVLAACR-A	VEEHNLITEGL	EDASAQAA	ARIJEGS RE	50
HUMANPRO.AMI	1	KLANAYNIS	SAVLATYGFL	VVANHEREEI	KOERAKDVE	VELESREKEE	50
		60	70	80	90	100	
MOUSEPRO.AMI	51	-GSQ <b>OF</b> F <b>E</b> LT	LEULTIOLER	LGSMERVLA	EVRTLKEAVD	SLKKSCODCK	100
HUMANPRO.AMI	51	EAGE Y VS	TEB PAIOTEK	FSRIDEVER	EVQNLKE I VN	<b>3LKKSCODCK</b>	100
		110	120	130	140	150	
MOUSEPRO.AMI	101	LOADDHRDPG	GNGGN	GAETAELS	CELESCVNKI	SSELKNAR	150
HUMANPRO.AMI	101	LOADDNEDPG	RNGLLLPSTG	APGEVGUNRV	RELESEVNKL	SSELKNAKEE	150
		160	170	180	190	200	
MOUSEPRO.AMI	151	HOGIOGREET	EHLVNMNNIE	NYVDNKVANL	TVVVNSLDGK	CSKCPSOEHM	200
HUMANPRO.AMI	151	INVLH GRUEK	CNLVNMNNIE	NYVDSKVANL	TEVVNSLDGK	CSKCPSOEOI	200
		210	220	230	240	250	
MOUSEPRO.AMI	201	<b>DSOPVOHLIY</b>	KDCSDHYVLG	RRSSGAYRVT	POHRNSSFEV	YCDMETMGGG	250
HUMANPRO.AMI	201	<b>PVQHLIY</b>	KDCSDYYAIS	HRSSETYRVT	PDPKNSSFEV	YCDMETMGGG	250
		260	270	280	290	300	
MOUSEPRO.AMI	251	NTVLQARLDG	STNETREME	YKAGFGNLER	<b>EFWLGNDKIH</b>	LLTKSKEMIL	300
HUMANPRO.AMI	251	<b>∦TVLQARLDG</b>	STRETPTACE	YKAGFGNLRP	EFWLGNDKIH	LLTKSKEMIL	300
		310	320	330	340	350	
MOUSEPRO.AMI	301	RIDLEDFNGL	TLYALYDOFY	VANEFLKYRL	HISNYNGTAG	DALRESPHYN	350
HUMANPRO.AMI	301	RIDLEDFNGV			HVGNYNGTAG	DALRENKHYN	350
		360	370	380	390	400	
MOUSEPRO.AMI	351	HDLRFFTTPD	RDNDRYPSGN	CGLYYSSGWW	FUSCLSANLN	<b>SKYYHOKY</b> KS	400
HUMANPRO.AMI	351					SKYYHQKY <mark>R</mark> S	400
		410	420	430	440	450	
MOUSEPRO.AMI	_	VRNGI FWGTW			MIRPKNEKP*		450
HUMANPRO.AMI	401	VRNGIFWGTW	PGVSEAHPGG	YKSSFKBAKM	MIRPK#FKP*		450

## <u>6/24</u>

		10	20	30	) 4(	50	
MOUSEPRO.AMI	1	MRLPGWLWLS	SAVLAACR-A	VEEHNLTEGI	EDASAOAACE	ARLEGSGRCE	50
HUMANPRO.AMI	1	MKLANWYWLS	SAVLATYGFL	VVANNETEEI	KDERAKDVC	VRLESRGKCE	50
		60					5(
MOUSEPRO.AMI	51	-GSQCPFQLT	LPTLTIQLPR	OLGSMEEVLK	EVRTLKEAVI	SLKKSCODCK	100
HUMANPRO.AMI	51	EAGECPYQVS	LPPLTIQLPK	OFSRIEEVFK	EVONIKETVN	SLKKSCQDCK	100
		110		130			100
MOUSEPRO.AMI	101	LQADDHRDPG	GNGGN	GAETAEDSRV		SSELKNAKDQ	
HUMANPRO.AMI	101	LQADDNGDPG	RNGLLLPSTG	APGEVGDNRV	RELESEVNKI.	SSELKNAKEE	150
		160	170	180			150
MOUSEPRO.AMI	151	IQGLQGRLET	LHLVNMNNIE			CSKCPSQEHM	200
HUMANPRO.AMI	151	INVLHGRLEK	LNLVNMNNIE	NYVDSKVANI.	TEVVNSLDGK	CSKCPSQEQI	200
		210	220	230	240	250	200
MOUSEPRO.AMI	201	QSQPVQHLIY					
HUMANPRO.AMI	201	QSRPVQHLIY	KDCSDYYAIG	KRSSETVRUT	DUDANGGEER	VCDMETMGGG	250
		260	270	280	290		250
MOUSEPRO.AMI	251	WTVLQARLDG				300	
HUMANPRO.AMI	251	WTVLQARLDG	STRETETWOO	YKAGEGNIEN	ELMTGNOVIU	LLENGKEMIL	300
		310	320	330	340		300
MOUSEPRO.AMI	301	RIDLEDFNGL				350	
HUMANPRO.AMI	301	RIDLEDFNGV	FLYALYDORY	ANDELINADI	HIGHYNCER	DALRESKHYN	350
		360	370	380			350
MOUSEPRO.AMI	351	HDLRFFTTPD			390	400	
HUMANPRO.AMI	351	HDLKFFTTPD	KUNDBADGCA	CCLTACCCEM	FDSCLSANLN	GKYYHQKYKG	400
	331	410	420				400
MOUSEPRO.AMI	401	- <del>-</del> -		430	440	450	
HUMANPRO.AMI		VRNGIFWGTW				• • • • • • • • • • •	450
	401	VRNGIFWGTW	PG V SEAH PGG	IKSSEKEAKM	MIRPKHEKP*		450

		10	20	30	40	50	60	70
	HKLYHMAM	LSSAVLA	YGFLVV	annetee ikdei	RAKDVCPVR	Lesrgkczea	SECPYOVSLI	PPLTIOLPK
HELIX	KHhhhhhhh	ռի <mark>ևևևև</mark> ի	ואממממממ	нинининии	thh		_	hh
SHEET	335333	333333			SSSSS	3	5333555	33355333
TURN		1	TTT	IIII		TITITIT		TTT TTT
COIL					c	cc	c	•••
		80	90	100	110	120	130	140
	QFSRIEEV	FKEVQNL	KEIVHSL	KKSCODCKLQA	DDNGDPGRN	GLLLPSTGAP	SEVGDNRVR!	ELESEUNET.
HELIX	<b>ТИННИННИ</b>							нинин
SHEET	32123333	338888	333333	352		3S3	*****	
TORN				TITTITIT TI			TTTTTT	
COIL								ccc
								CCC
	1	.50	160	170	180	190	200	210
	SSELKNAK	œeinvlh	GRLEKT.N	LVNHNNIENYV				210
HELIX	нининн	THKhhhh	hhh##hh	hhhh	hhhhhh			
SHEET		5553		222222222				հիհիհիհի
TURH			TTT		TTTT	ITTTTTT		\$333533 <u>3</u>
COIL	cc	•	•••			1111111	LITTT	Ī
	-							
		220	230	240	250	260	270	
	_			PKNSSFEVYCD				280
HELIX	h					րրը Մարդերի	pppH werktwoni	
						HITTHITICIE!	ณกกก	ннк
SHEET	2 2:	33	35553	- 4454		20000		
		3S TTTTT		355555 TTTTTT		355555	55533	*
	IIIIIII			≥\$\$\$\$\$ TTTTTT	SSS 35	SSSSSS TITTT		_
TURN								T CCCCC
TURN	1111111			TITTI	TITTIT	TITIT	TT TTTT	cccc
TURN	TITITIT	TTTTT1	300	310	320	77 <b>77</b> 7	TT TTTT 340	CCCCC 350
TURN	TITITIT	TTTTTT 290 KIHLLTKS	300 SKEMILRI	TITITI 310 (Dledfhgvel)	TIITTI  320 (ALYDQFYV)	330 LHEFLKYRLHV	TT TTTT 340	CCCCC 350
TURN COIL HELIX	TITITIT	TTTTTT 290 KIHLLTKS	300 SKEMILRI	TTTTTT 310 DLEDFNGVELY DHHHDDDDDD	TTITTT  320 (ALYDQFYV)	TITIT 330 ANEFLKYRLKV SABBBB	TT TTTT 340 GNYNGTAGD	CCCCC 350
TURN COIL HELIX	TITITITI  EFWLGHD	TTTTTT 290 KIHLLTKS hhhhhhh SSSS:	300 SKEMILRI SHBBBBB SSSS	310 (Dledfrgvel) hhhhhhhhhhh 533 S\$SS	TTITTT  320 (ALYDQFYV)	TITIT 330 ANEFLKYRLHV bhhhhH SSSSSSSSS	TT TTTT 340 GHYNGTAGD	SECCE 350 ALRENKHYN
TURN COIL HELIX SHEET	TITITIT  EFWLGND  ( HHHh	TTTTTT 290 KIHLLTKS hhhhhhh SS <b>SS</b> 3	300 SKEMILRI SHBBBBB SSSS	TTTTTT 310 DLEDFNGVELY DHHHDDDDDD	TTITTT  320 (ALYDQFYV)	TITIT 330 ANEFLKYRLHV bhhhhH SSSSSSSSS	TT TTTT  340 GHYNGTAGD	CCCCC 350 ALRENKHYN TITIT
TURN COIL RELIX SHEET TURN	TITITIT  EFWLGND  ( HHHh	TTTTTT 290 KIHLLTKS hhhhhhh SS <b>SS</b> 3	300 SKEMILRI SHBBBBB SSSS	310 (Dledfrgvel) hhhhhhhhhhh 533 S\$SS	TTITTT  320 (ALYDQFYV)	TITIT 330 ANEFLKYRLHV bhhhhH SSSSSSSSS	TT TTTT  340 GHYNGTAGD	SECCE 350 ALRENKHYN
TURN COIL RELIX SHEET TURN	EFWLGND: CHNHh SSSS TITT	TTTTTT 290 KIHLLTKS hhhhhhh SS <b>SS</b> 3	300 SKEMILRI SHBBBBB SSSS	310 (DLEDFNGVEL) hhhhhhhhhhhh 5S3 S\$SS	320 (ALYDOFYV) hhhhhhhhh ssssssss	TITIT 330 Weflkyrlhv Dhhhhh Ssssssssss Ti	TT TTTT  340 GHYNGTAGD	CCCCC 350 ALRENKHYN TITIT
TURN COIL RELIX SHEET TURN	EFWLGND:	TTTTTT  290 KINLITKS hhbbbhh SSSS T TTT	300 SKEMILRI SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	310 DLEDFRGVELY SHHHADADADA SSS SSSS TTTT	320 (ALYDQFYV) shhhhhhhhh ssssssss	TITIT  330 ANEFLKYRLHV SSSSSSSSSSSSST TI	340 GHYNGTAGD	350 ALRENKHYN TITIT CCCC
TURN COIL HELIX SHEET TURN COIL	EFWLGND:	TTTTTT  290 KIHLLTKS hhhhhhhh SSSS T TTT  360 TPDKDND	300 SKEMILRI SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	310 IDLEDFNGVELY ABHHADADADA SSS SSSS TITT  380 GLYYSSGWWFD	320 (ALYDOFYV) Abbbbbbb SSSSSSSSSSSSSSSSSSSSSSSSSSSSS	TITIT  330 ANEFLKYRLHV SSSSSSSSSSSSST TI	340 GHYNGTAGD TITTITITI 410 CHGIFHGIRE	350 ALRENKHYN TITIT CCCC 420 CGVSEAHPGG
TURN COIL HELIX SHEET TURN COIL	EFWLGHD: ( HHHh : ) ( SSS TITT  HOLKFFT X hhhhhh	TTTTTT  290 KIHLLTKS hhhhhhhh SSSS T TTT  360 TPDKDNDI	300 SKEMILRI SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	310 IDLEDFNGVELY ANHHANNANNAN SSS SSSS TITT  380 GLYYSSGWWFDI	320 (ALYDOFYV) Ahhhhhhhhh BSSSSSSSSSSSSSSSSSSSSSSSSSSS	JJO NEFLKYRLHV SSSSSSSSSS TI 400 KYYHQKYRGVE	340 GHYNGTAGD TTTTTTTTT  410 RHGIFWGIWE	350 ALRENKHYN TITIT CCCC 420 CVSEAHPGG
TURN COIL HELIX SHEET TURN COIL HELIX	EFWLGHD: ( HHHh :	TTTTTT  290 KIHLLTKS hhhhhhhh SSSS T TTT  360 TPDKDNDI h	300 SKEMILRI SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	310 IDLEDFNGVELY ABHBABABABA SSS SSSS TITT  380 GLYYSSGWWFDI ABB	320 (ALYDOFYV) Abbabababa SSSSSSSSSSSSSSSSSSSSSSSSSSSS	JJO NEFLKYRLHV SSSSSSSSS TI 400 KYYHQKYRGVI	340 CHYNGTAGE TTTTTTTTT  410 CHGIFWGTWE	350 ALRENKHYN TITIT CCCC 420 CGVSEAHPGG
TURN COIL HELIX SHEET TURN COIL HELIX SHEET	EFWLGHD: ( HHHh :	TTTTTT  290 KIHLLTKS hhhhhhhh SSSS T TTT  360 TPDKDNDI h	300 SKEMILRI SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	310 IDLEDFNGVELY ABHBABABABA SSS SSSS TITT  380 GLYYSSGWWFDI ABB	320 (ALYDOFYV) Ahhhhhhhhh BSSSSSSSSSSSSSSSSSSSSSSSSSSS	JJO NEFLKYRLHV SSSSSSSSS TI 400 KYYHQKYRGVI	340 CHYNGTAGE TTTTTTTTT  410 CHGIFWGTWE	350 ALRENKHYN TITIT CCCC 420 CVSEAHPGG
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN	EFWLGHD: ( HHHh :	TTTTTT  290 KIHLLTKS hhhhhhhh SSSS T TTT  360 TPDKDNDI h	300 SKEMILRI SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	310 IDLEDFNGVELY ABHBABABABA SSS SSSS TITT  380 GLYYSSGWWFDI ABB	320 (ALYDOFYV) Abbabababa SSSSSSSSSSSSSSSSSSSSSSSSSSSS	JJO NEFLKYRLHV SSSSSSSSS TI 400 KYYHQKYRGVI	340 CHYNGTAGE TTTTTTTTT  410 CHGIFWGTWE	350 ALRENKHYN TITIT CCCC 420 CGVSEAHPGG
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN	EFWLGHD: ( HHHh :	TTTTTT  290 KIHLLTKS hhhhhhhh SSSS T TTT  360 TPDKDNDI h	300 SKEMILRI SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	310 IDLEDFNGVELY ABHBABABABA SSS SSSS TITT  380 GLYYSSGWWFDI ABB	320 (ALYDOFYV) Abbabababa SSSSSSSSSSSSSSSSSSSSSSSSSSSS	JJO NEFLKYRLHV SSSSSSSSS TI 400 KYYHQKYRGVI	340 CHYNGTAGD TTTTTTTTT  410 CHGIFWGTWE	350 ALRENKHYN TITIT CCCC 420 CGVSEAHPGG
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN	EFWLGND: ( HHHh :	TTTTTT  290 KIHLLTKS hhbhbhhi SSSS T TTT  360 TPDKDNDI h STTTTTTTT	300 SKEMILRI SHANNAN SSSSIT 370 RYPSGNC	310 IDLEDFNGVELY ABHBABABABA SSS SSSS TITT  380 GLYYSSGWWFDI ABB	320 (ALYDOFYV) Abbabababa SSSSSSSSSSSSSSSSSSSSSSSSSSSS	JJO NEFLKYRLHV SSSSSSSSS TI 400 KYYHQKYRGVI	340 CHYNGTAGD TTTTTTTTT  410 CHGIFWGTWE	350 ALRENKHYN TITIT CCCC 420 CGVSEAHPGG
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN	EFWLGHD ( HHHh ) ssss TITT  HDLKFFT X hhhhhh I sssss ITT	TTTTTT  290 KIHLLTKS hhhhhhhh SSSS T TTT  360 TPDKDNDI h S	300 SKEMILRI SHANNAN SSSSIT 370 RYPSGNC	310 IDLEDFNGVELY ABHBABABABA SSS SSSS TITT  380 GLYYSSGWWFDI ABB	320 (ALYDOFYV) Abbabababa SSSSSSSSSSSSSSSSSSSSSSSSSSSS	JJO NEFLKYRLHV SSSSSSSSS TI 400 KYYHQKYRGVI	340 CHYNGTAGD TTTTTTTTT  410 CHGIFWGTWE	350 ALRENKHYN TITIT CCCC 420 CGVSEAHPGG
TURN COIL RELIX SHEET TURN COIL HELII SHEET TURN COIL	EFWLGHD ( HHHh ) ssss TITT  HDLKFFT X hhhhhh ssssss TIT  YKSSFKE X hhe	TTTTTT  290 KIHLLTKS hhhhhhhi SSSS T TTT  360 TPDKDNDI h S TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	300 SKEMILRI SHANNAN SSSSIT 370 RYPSGNC	310 IDLEDFNGVELY ABHBABABABA SSS SSSS TITT  380 GLYYSSGWWFDI ABB	320 (ALYDOFYV) Abbabababa SSSSSSSSSSSSSSSSSSSSSSSSSSSS	JJO NEFLKYRLHV SSSSSSSSS TI 400 KYYHQKYRGVI	340 CHYNGTAGD TTTTTTTTT  410 CHGIFWGTWE	350 ALRENKHYN TITIT CCCC 420 CGVSEAHPGG
TURN COIL RELIX SHEET TURN COIL HELIX SHEET TURN COIL	EFWLGHD ( HHHh ) ssss TITT  HDLKFFT X hhhhhh ssssss TITT  YKSSFKE X hhe	TTTTTT  290 KIHLLTKS hhhhhhhi SSSS T TTT  360 TPDKDNDI h S TTTTTTTT  430 CARPMIRP HHHHHH SSS	300 SKEMILRI SHANNAN SSSSITT 370 RYPSGNCI	310 IDLEDFNGVELY ABHBABABABA SSS SSSS TITT  380 GLYYSSGWWFDI ABB	320 (ALYDOFYV) Abbabababa SSSSSSSSSSSSSSSSSSSSSSSSSSSS	JJO NEFLKYRLHV SSSSSSSSS TI 400 KYYHQKYRGVI	340 CHYNGTAGD TTTTTTTTT  410 CHGIFWGTWE	350 ALRENKHYN TITIT CCCC 420 CGVSEAHPGG
TURN COIL RELIX SHEET TURN COIL HELII SHEET TURN COIL	EFWLGND ( HHHh ) ssss TITT  HDLKFFT X hhhhhh sssss TIT  YKSSFKE X hhe T	TTTTTT  290 KIHLLTKS hhhhhhhi SSSS T TTT  360 TPDKDNDI h S TTTTTTTT  430 CARPMIRP HHHHHH SSS	300 SKEMILRI SHANNAN SSSSIT 370 RYPSGNC	310 IDLEDFNGVELY ABHBABABABA SSS SSSS TITT  380 GLYYSSGWWFDI ABB	320 (ALYDOFYV) Abbabababa SSSSSSSSSSSSSSSSSSSSSSSSSSSS	JJO NEFLKYRLHV SSSSSSSSS TI 400 KYYHQKYRGVI	340 CHYNGTAGD TTTTTTTTT  410 CHGIFWGTWE	350 ALRENKHYN TITIT CCCC 420 CGVSEAHPGG

### <u>8/24</u>

		10	2.0			_	
MOUSEPRO.DNA	1						
HUMANPRO.DNA	1	TACCOTTOGA	ACCALCEMEN	TG-GAATGAG	AAGGGA-AAG	TAGGAGCCCG	50
	1	1AGGGIIGGA 60		CCTGAGTATG			50
MOUSEPRO.DNA	51			80 GCATAAGGCG			
HUMANPRO.DNA	51	CARCTCTARA	CACTCTCCCA	ACATTTTGAG	TGTCTGACAA	ATTCTTCATA	100
	31	110	120				100
MOUSEPRO.DNA	101			130 ATTCAGTCTG	140		
HUMANPRO.DNA	101	TA-ADATTA	CCCTITGCAC	AGAAAAGTCA	TATAGGTTAT	TTCTATAGGA	150
	101	160	170	180			150
MOUSEPRO.DNA	151			CTTGTGCACT	190	200	
HUMANPRO. DNA	151	ATAAATATCA	GATAGGCTAC	AGAGTGTTTT	G-GIAACAGG	CATGAAGGCT	200
		210	220	230	240	250	200
MOUSEPRO.DNA	201			ATGTCCAGTT			252
HUMANPRO.DNA				A-GTCATTTT			250
		260	270	280	290	300	250
MOUSEPRO. DNA	251			GAAAGTGCGC			300
HUMANPRO. DNA				AGAAATCTTA			300 300
		310	320	330	340	350	300
MOUSEPRO. DNA	301			CAGTTA			350
HUMANPRO. DNA	301	CAAATTAAAA	GGAGGTGGTT	TCTCTAACTG	AAGCTGTTCC	TCTTTCCTCC	350
		360	370	380	390	400	330
MOUSEPRO. DNA	351	AAAGTCTT	GGGAAATCTG	GTTAGAGA			400
HUMAN PRO. DNA	351	CTTCAGCCTC	TGAAGAGAAA	GTTAGAAAAC	TATTATCATT	AATGCTACAT	400
		410	420	430	440	450	
MOUSE PRO. DNA	401	ATGGTGGTAC	ACACCTGTGA	TCTCTGTGTT	TAGGAGGGAG	AGGCAGAGAG	450
HUMANPRO. DNA				ACCAAGTGGC			450
		460	470	480	490	500	
MOUSE PRO. DNA	451	ATCAGGAGTT	CAAGGCCAGC	CTGAGCTACT	TGAGACCCAG	TCTAAATAAA	500
HUMAN PRO. DNA	451	ACCAGCG	TGGAGACAGA	AAGCAA	-GAGGCCC-G	CCTGCCAGGG	500
		510	520	530	540	550	
MOUSE PRO. DNA	501	TAAGAGATAG	ATTACAGAGT	GCCTTTAACT	AGTACAGAGA	AAGAATTTGG	550
HUMAN PRO. DNA	501	CTACCTGCAG	AA-AGAAAGG	GCAAAGATGC	TGTAGGCAAG	AGAAGTTCAG	550
		560	570	580	590	600	
MOUSE PRO. DNA				CTGAAATAAT			600
HUMAN PRO. DNA	551		GGCATA-G	CTCAAA-GAT	T.CACATTTGA	GCAGC	600
W0000000000000000000000000000000000000		610	620	630	640	650	
MOUSEPRO.DNA				G-GTCAGTAT			650
HUMANPRO.DNA	601			TTACCAAAAT		CAAAGGAG	650
MOUSEPRO.DNA		660	670	680	690	700	
HUMANPRO.DNA				GTGATGGGGA			700
HOMANERO. DNA	651			-TGATGA		TGTCCTTT	700
MOUSEPRO.DNA	701	710	720	730	740	750	
HUMAN PRO. DNA	701	TGTGTGAGTG	ACGTGCTTCC	AAGTGTTTTA .	ACCACTGACG	ATTACATAGC	750
	701	760		AGACATTTAT .			750
MOUSEPRO.DNA	751		770	780	790	800	
HUMAN PRO. DNA				AGCCGTATTC A-CTTTTTC			800
	, 3 1	810	AGAAAGTAGC 820				800
MOUSEPRO.DNA	803			830 CACACAGAGA	840	850	25.5
HUMAN PRO. DNA				AGT-CAACTG			850
	301	860	870	AGI-CAACIG 880	CAATAGTCAG . 890		850
		000	3,0	350	050	900	

WO 98/51335 PCT/CA98/00475

### 9/24

# FIGURE 8 cont'd

MOUSEPRO.DNA	851	TTTGTTCTGA	TTAGGGGCAA	TTTTAAGTAC	TTAAGAGTTC	ACACAAAGTC	900
HUMANPRO.DNA	851	TTTGTTACAC	TTAGAAACTT	CTAAAAGTGC	TTAAGATTTC	ACCTGAAAGT	900
		910		930			200
MOUSEPRO.DNA		TAGCCTTCAA					950
HUMAN PRO. DNA	901	CCAACAT-GA	AGAAAATACA	GGCTCCCCAA	TGCCCCATTC	TAAGAAGAAA	950
		960	970	980	990		
MOUSEPRO.DNA						GCTCACAGAC	1000
HUMANPRO.DNA	951	AAGGACCATT	TTCATTTTAG	TAACGTTTCT	GTTCTATAGA	CAGTTTGGAT	1000
		1010	1020	1030	1040	1050	
MOUSEPRO.DNA		ATTTAGACGT					1050
HUMAN PRO . DNA	1001	AACTAGCTCT	TACTTTTTAT	CTTTAAAAAC	TGTTTTTCCA	GTGAAGTTAC	1050
		1060	1070	1080	1090	1100	
MOUSEPRO.DNA	1051	ATAATATGGT	ATCTTTTGGG	CACTGGTATT	ACAA-CTGTT	TTTTAAACAA	1100
HUMANPRO.DNA	1051	GTATAATTAT	TTACTTCAAG	CG-TAGTATA	CCAAATTACT	TTAGAAATGC	1100
		1110	1120	1130	1140	1150	
MOUSEPRO.DNA	1101	AAGACTTTCC	TTGTGCTTTA	CTAAAAAC-C	CA-GACGGTG	AATCTTGAAT	1150
HUMANPRO.DNA	1101	AAGACTTTTC	TTATACTTCA	TAAAATACAT	TATGAAAGTG	AATCTTGT	1150
		1160	1170	1180	1190	1200	
MOUSEPRO.DNA		ACAATGCGTG					1200
HUMANPRO.DNA	1151	TGGCTGTGTA	CATTTGACTA	TAATAATTTC	AATGCATATT	ATTTCTATTG	1200
		1210	1220	1230	1240	1250	
MOUSEPRO.DNA		ACAGGAGATG					1250
HUMANPRO.DNA	1201	AGAGTAAGTT	ACAGTTTTTG	GCAAACTGCG	TTTGATGAGG	GCTATCTCCT	1250
		1260	1270	1280	1290	1300	
MOUSEPRO.DNA				CT-GTGATGC			1300
HUMAN PRO. DNA	1251		GTTTCTAAAA	CTTGTGATGC	AAACGCTCCC	ACCCTTTCCT	1300
		1310	1320	1330	1340	1350	
MOUSEPRO.DNA		GGGAACTCAG					1350
HUMANPRO.DNA	1301	GGGAACACAG			GCCGCTATTA	AAGCAGCTCC	1350
		1360	1370	1380	1390	1400	
MOUSEPRO. DNA		CCTGGTC					1400
HUMAN PRO. DNA	1351	AGCCCTGCGC	ACTCCCTGCT	GGGTGAGCAG	CACTGTAAAG	ATG	1400

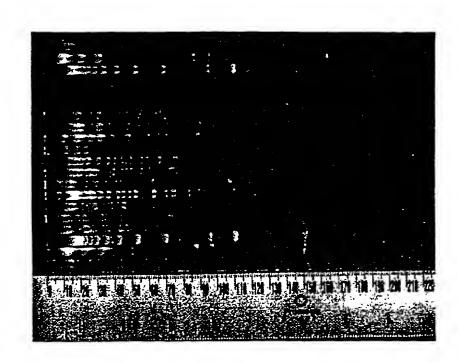
		LIGU	KE 9		
18	)	20	30	40	50
TAGGGTTGG	AAGCCAGG	STCTCCT	GAGTATGCGAG	AATAAATACA	GTCATG
60		70	80	90	100
			TTTTGAGAATG	TGAATAGGAT	TTGGCT
110		120	130	140	150
AAAATTAAGO	GGATATA		agtcat <u>aggaa</u>	ATCAGGTTAA	AGACAT
		TCF1			
160		170	180	190	200
			GTT <u>TTAAGTAA</u>	TACAATAAAA	CATTTA
210	ATA1	220	NF IL6 230	240	250
			230 <u>ITGAAAT</u> TATT	240	250
GATTITIGE	CRIGICE		F IL6	IIIAAAGCAA	AAAAAC
260		270	280	290	300
CCTTTTTAAA	ACAAGAAA	TCTTAT	GAGATGTCAAT	ATGCAAAACA	AATTAA
31	0	320	330	340	350
	GTTTCTC	TAACTGA	AGCTGTTCCT	CTTTCCTGCC	TTCAGCC
TCF1	•	0.00	222	200	400
36			380		400
TUTGAAGAG	AAAGIIA		TATTATCATTA F_E1	AIGCIACAIG	IIIIGAA
41	0		430	440	450
CAAGCTGAT	ATAC <u>CAA</u>	<u>GTG</u> GCCC	CAGAGAGCAGG	ragaagaacc	AGCGTGG
	ЬHI				
46	=	470		490	500
AGACAGAAA	GCAAGAG	GCCCGCC	CTGCCAGGGCT		-
		<b>500</b>	500	NF IL6	
51		520			550
TCF1	C161A66	CAAGAGA	AGTTCAGGAC	AGACAC I GGC	ATAGCIL
56	0	570	580	590	600
:AAAGATTCA	CATTIGA	GCAGCTO	TGGAAGATGA	CAGTACAATT	ACCAAAA
TCF1	ЬНLН	<b>bHLH</b>			
		E2A			
61		620	630	640	650
TGTCGAAGG		AGGCAG	CTACTGGTTT <u>T</u>		AATTATG
	TCF1	670	600	NF ILE	700
66	-	670	680 ATTTAGACATT	690	700
	LO	720	730	740	750
	-		ACTTTTTTCTC		
TCF1	Jan i Hurf	ino i ngc.	aci i i i i i i i i i i i i i i i i i i	CHCINGIIII	Citotol
	60	770	780	790	800
TTTTCAAG	TAGATGA		GTCAACTGCAA	TAGTCAGAAA	GCTGTAC
	GYTTA CE-		bhlh		-
	SUBSTI	TUTE SH	EET (RULE 26	)	

# FIGURE 9 CONT'D

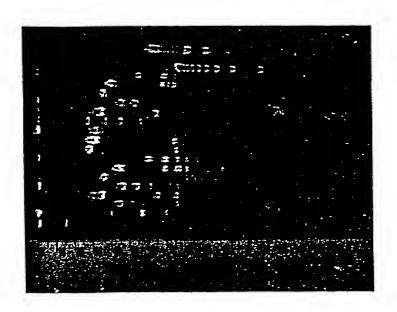
	_			
810	820	830		850
TTTGTTACACTTAG	SAAACTTCTA	AAAGTGCTTA	AGATTT <u>CACC</u>	TGAAACG
		CF1	bHL	
860	870	880	890	900
CCAACATGAAGAAA	ATACAGGCT	CCCCAATGCC	CCATTCTAAG	AAGAAAA
910	920	930	940	950
AGGACCATTTTCAT	TTTAGTAAC	GTTTCTGTTC		TTGGATA
960		980	990	1000
ACTAGCTCTTACTT	TTTATCTTT	AAAAACTGTT		AGTTACO
1010	1020	1030		1050
TATAATTATTTACT	TCAAGCGTA			
			NF I	
1060	1070	1080		1100
GACTTTTCTTATAC				TCTTCCC
		NF ILE		1011660
1110	1120			1150
TGTGTACATTTGAC				
bHLH:		CHRIGORIE	HILLICIA	LIGAGAG
	1170	1180	1190	1200
TAAGTTACAGTTTT				
1210	1220	1230		
CTGTGCGTTTCTAA				1250
O. O. O. O. O. I. I. C. I. R.	AAE		CCACCCITI	JC I GGGA
1260	1270	<del>-</del>		
			1290	1300
ACACAGAAACGCTG	ALILBUGAL	TELESCOCIAL AT	LAAAGCAGC	ICCAGCC
+1 AP		TATA	xod a	
1310			•	
CTGCGCACTCCCTG	الـ <u>ا</u> لحاجات الـ AG(	LAGCACTGTAA	AGATG	

# FIGURE 10A

### 12/24



# FIGURE 10B



13/24

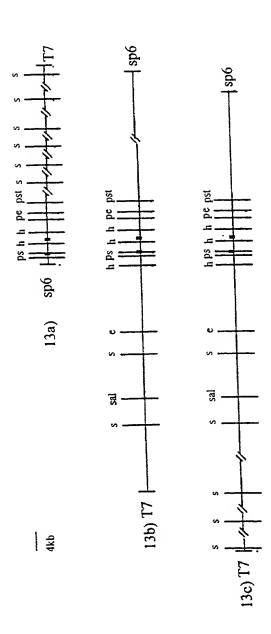
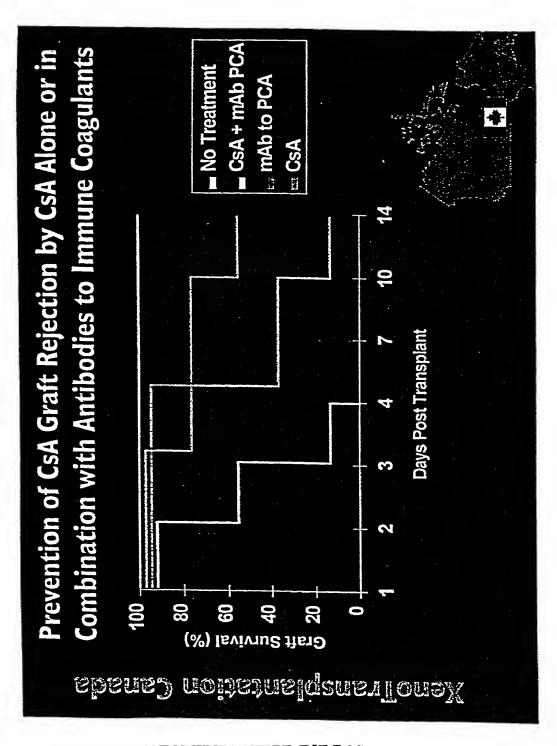
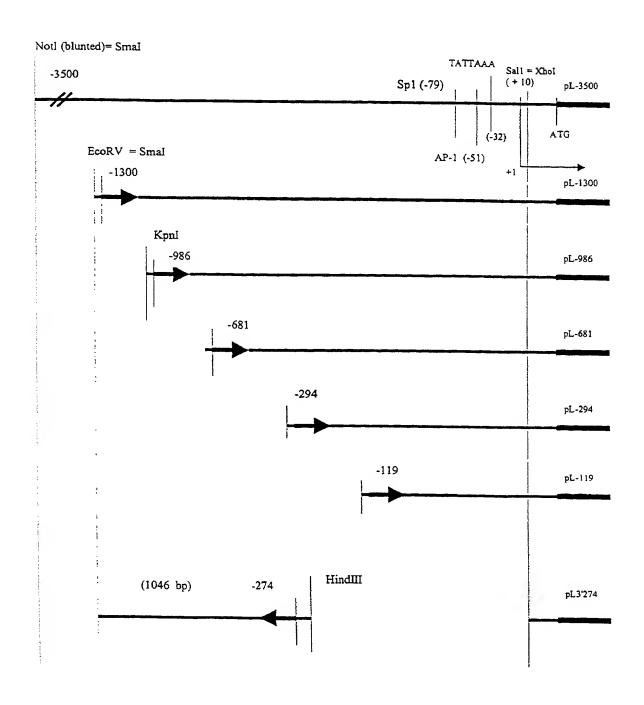


FIGURE 12

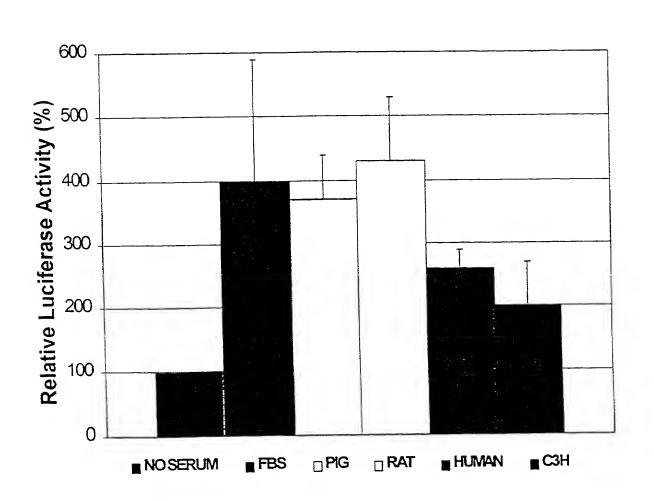
14/24



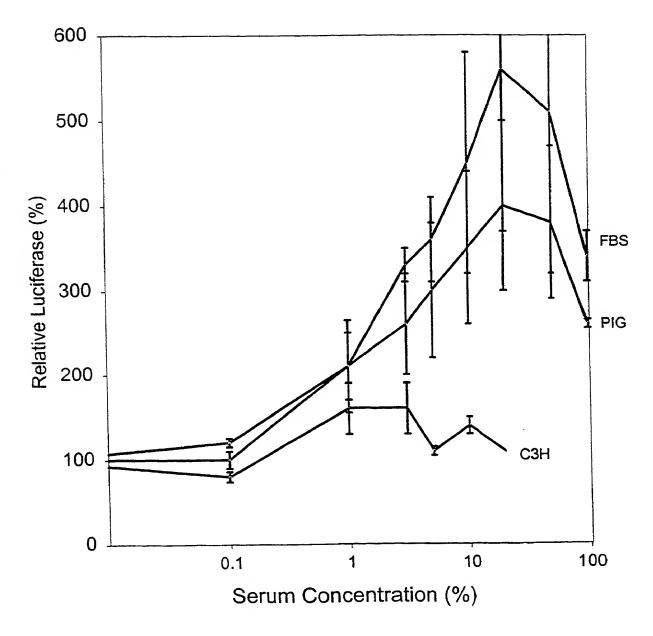
15/24 FIGURE 13



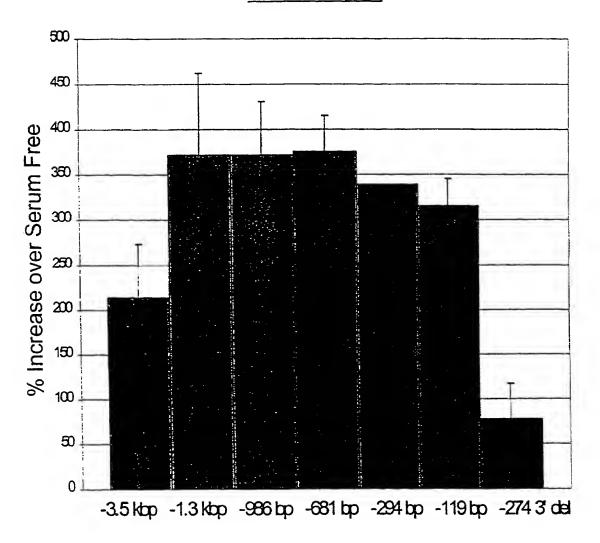
16/24



17/24 FIGURE 15



SUBSTITUTE SHEET (RULE 26)



### FIGURE 17

5'-- CCAAGTATAT AATATGGTAT CTITTGGGCA CTGGTATTAC AACTGTTTTT -270

TAAACAAAAG ACTTTCCTTG TGCTTTACTA AAAACCCAGA CGGTGAATCT -220

TGAATACAAT GCGTGGCACC CACGGCAGGCATTCTATTGT GCATAGTTTT -170

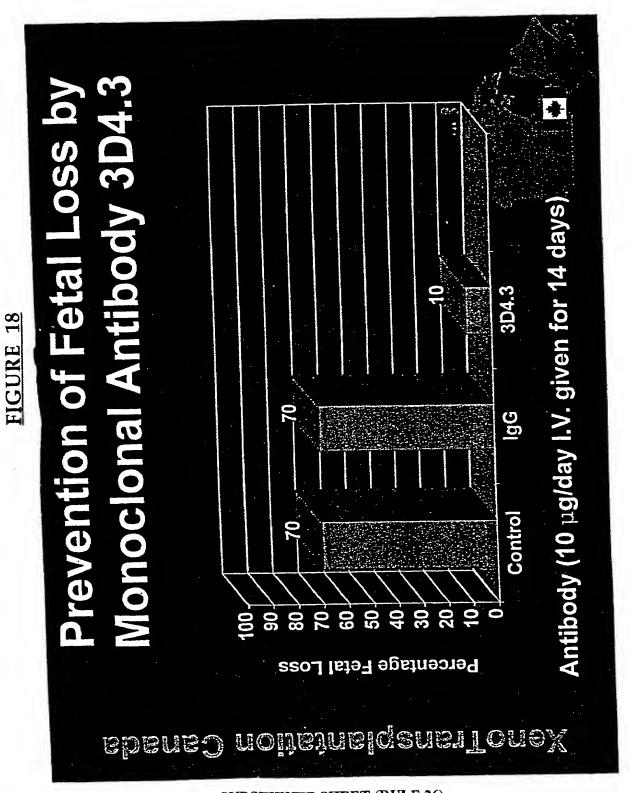
GACTGACAGG AGATGACAGC ATTTGGCTGC GTGCGCTTGC TGAGGACCCT -120

CTCCTCCTGT GTGGCGTCTG AGACTGTGAT GCAAATGCGC CCGCCCTTTT -70

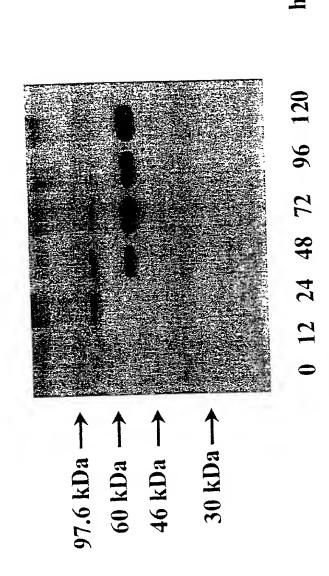
CTGGGAACTC AGAANGCCTG AGTCAGGCGG CGGTGGCTAT TAAAGCGCCT -20

GGTCAGGCTG GGCTGCCGCA CTCCAAGG--3'

+1



21/24

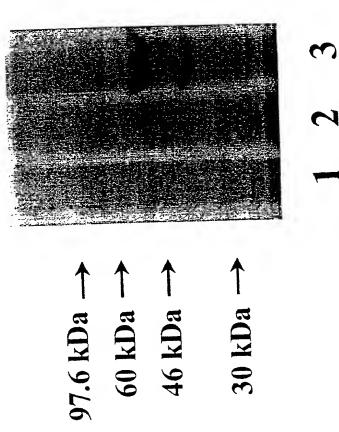


The lanes are: 1. H5cells

H5 + wild type virus H5 + recombinant

97.6 kDa · 60 kDa ·

The lanes are:
1. H5cells
2. H5 + wild type virus
3. H5 + recombinant
virus



The lanes are:

1. <sup>125</sup>I-Prothrombin (PT)
 2. PT +RVV + Factor X
 3. PT +H5
 4. PT + H5-RV
 5. PT + purified protein (3 μg)

